FIG. 1

ATGTTCTTTCTACTTCATTTCATCGTTCTGATCAATGTCAAAGATTTTGCACTGACTCAA
GGTAGCATGATCACTCCTTCATGCCAAAAAGGATATTTTCCCTGTGGGAATCTTACCAAG
TGCTTACCCCGAGCTTTTCACTGTGATGGCAAGGATGACTGTGGGAACGGGGCGGACGAA
GAGAACTGTGGTGACACTAGTGGATGGGCGACCATATTTGGCACAGTGCATGGAAATGCT
AACAGCGTGGCCTTAACACAGGAGTGCTTTCTAAAACAGTATCCACAATGCTGTGACTGC
AAAGAAACTGAATTGGAATGTGTAAATGGTGACTTAAAGTCTGTGCCGATGATTTCTAAC
AATGTGACATTACTGTCTCTTAAGAAAAACAAAATCCACAGTCTTCCAGATAAAGTTTTC
ATCAAATACACAAAACTTAAAAAGATATTTCTTCAGCATAATTGCATTAGACACATATCC
AGGAAAGCATTTTTTGGATTATGTAATCTGCAAATATTATATCTCAACCACAACTGCATC
ACAACCCTCAGACCTGGAATATTCAAAGACTTACATCAGCTAACTTGGCTAATTCTAGAT
GACAATCCAATAACCAGAATTTCACAGCGCTTGTTTACGGGATTAAATTCCTTGTTTTTC
CTGTCTATGGTTAATAACTACTTAGAAGCTCTTCCCAAGCAGATGTGTGCCCAAATGCCT
CAACTCAACTGGGTGGATTTGGAAGGCAATAGAATAAAGTATCTCACAAATTCTACGTTT
CTGTCGTGCGATTCGCTCACAGTGCTGTTTCTGCCTAGAAATCAAATTGGTTTTGTTCCA
GAGAAGACATTTTCTTCATTAAAAAATTTAGGAGAACTGGATCTGTCTAGCAATACGATA
ACGGAGCTATCACCTCACCTTTTTAAAGACTTGAAGCTTCTACAAAAGCTGAACCTGTCA
TCCAATCCTCTTATGTATCTTCACAAGAACCAGTTTGAAAGTCTTAAACAACTTCAGTCT
CTAGACCTGGAAAGGATAGAGATTCCAAATATAAACACACGAATGTTTCAACCCATGAAG
AATCTTTCTCACATTTATTTCAAAAACTTTCGATACTGCTCCTATGCTCCCCATGTCCGA
ATATGTATGCCCTTGACGGACGGCATTTCTTCATTTGAGGACCTCTTGGCTAACAATATC
CTCAGAATATTTGTCTGGGTTATAGCTTTCATTACCTGCTTTGGAAATCTTTTTGTCATT
GGCATGAGATCTTTCATTAAAGCTGAAAATACAACTCACGCTATGTCCATCAAAATCCTT
TGTTGTGCTGATTGCCTGATGGGTGTTTACTTGTTCTTTGTTGGCATTTTCGATATAAAA
TACCGAGGGCAGTATCAGAAGTATGCCTTGCTGTGGATGGAGAGCGTGCAGTGCCGCCTC
ATGGGGTTCCTGGCCATGCTGTCCACCGAAGTCTCTGTTCTGCTACTGACCTACTTGACT
TTGGAGAAGTTCCTGGTCATTGTCTTCCCCTTCAGTAACATTCGACCTGGAAAACGGCAG
ACCTCAGTCATCCTCATTTGCATCTGGATGGCGGGATTTTTAATAGCTGTAATTCCATTT
TGGAATAAGGATTATTTTGGAAACTTTTATGGGAAAAATGGAGTATGTTTCCCACTTTAT
TATGACCAAACAGAAGATATTGGAAGCAAAGGGTATTCTCTTGGAATTTTCCTAGGTGTG
AACTTGCTGGCTTTTCTCATCATTGTGTTTTCCTATATTACTATGTTCTGTTCCATTCAA
AAAACCGCCTTGCAGACCACAGAAGTAAGGAATTGTTTTGGAAGAGAGGTGGCTGTTGCA
AATCGTTTCTTTTTTATAGTGTTCTCTGATGCCATCTGCTGGATTCCTGTATTTGTAGTT
AAAATCCTTTCCCTCTTCCGGGTGGAAATACCAGACACAATGACTTCCTGGATAGTGATT
TTTTTCCTTCCAGTTAACAGTGCTTTGAATCCAATCCTCTATACTCTCACAACCAACTTT
TTTAAGGACAAGTTGAAACAGCTGCTGCACAAACATCAGAGGAAATCAATTTTCAAAATT
AAAAAAAAAAGTTTATCTACATCCATTGTGTGGATAGAGGACTCCTCTTCCCTGAAACTT
GGGGTTTTGAACAAAATAACACTTGGAGACAGTATAATGAAACCAGTTTCCTAG

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FIG.2

MFFLLHFIVLINVKDFALTQGSMITPSCQKGYFPCGNLTKCLPRAFHCDGKDDCGNGADE
ENCGDTSGWATIFGTVHGNANSVALTQECFLKQYPQCCDCKETELECVNGDLKSVPMISN
NVTLLSLKKNKIHSLPDKVFIKYTKLKKIFLQHNCIRHISRKAFFGLCNLQILYLNHNCI
TTLRPGIFKDLHQLTWLILDDNPITRISQRLFTGLNSLFFLSMVNNYLEALPKQMCAQMP
QLNWVDLEGNRIKYLTNSTFLSCDSLTVLFLPRNQIGFVPEKTFSSLKNLGELDLSSNTI
TELSPHLFKDLKLLQKLNLSSNPLMYLHKNQFESLKQLQSLDLERIEIPNINTRMFQPMK
NLSHIYFKNFRYCSYAPHVRICMPLTDGISSFEDLLANNILRIFVWVIAFITCFGNLFVI
GMRSFIKAENTTHAMSIKILCCADCLMGVYLFFVGIFDIKYRGQYQKYALLWMESVQCRL
MGFLAMLSTEVSVLLLTYLTLEKFLVIVFPFSNIRPGKRQTSVILICIWMAGFLIAVIPF
WNKDYFGNFYGKNGVCFPLYYDQTEDIGSKGYSLGIFLGVNLLAFLIIVFSYITMFCSIQ
KTALQTTEVRNCFGREVAVANRFFFIVFSDAICWIPVFVVKILSLFRVEIPDTMTSWIVI
FFLPVNSALNPILYTLTTNFFKDKLKQLLHKHQRKSIFKIKKKSLSTSIVWIEDSSSLKL
GVLNKITLGDSIMKPVS

FIG. 3

CCACGCGTCCGATTACA

FIG. 4

CAATCATTTTGGATCACTGGACTTTCAGTGGACTACCTAAAACAGGGGACAGCTTTTGGA
AGATGACATCTGCAATGCTTTTCATCTTTACCAACGGCAAGCCTTTCTGCACAGAGAGCA
CAGCAGAATGGCTCCTGTCACTGCATTCCAATGGCAGCTGTACTATCTACCAACCGTGCT
GAGGACAGCACCAAAGGTTCCTCTCCTCACCCCACATGCCTGAAAAGCACATGTGAATTC
GTGTATAGTGGGCTGAGGTGCAGCTGATCTCTAGCTAATCAACACAACCCACCAACAAAT
GACCACAGGTTGGCACTGTGTGGTCTTTCACATCGGGTTGCACTGTCCATGAAATAGAAA
CACTCACAACATCTGATTCCAGTGTGGCCATAATAACAGAAATCTAACAACTCTTTCCTT
GCCTTTTCAATATCAAATAAAACCATCAGCATCCTGCTGGATTGATAGCAAAGGATTTCC
AAAATATTCATCTACCCGAAGTCCTCCTCTGTGAAGGCCGGTGGAGTAGCCACTTTGAAA
ACAGAACTTCCAACCAGGTTACCATGTCTAACCTATGACCAGAGAGTCACACTGATGAAG
CCTCATACCATTTGCCTTTTGGATTTTATTTAATATCAGAAGAGATGAATTCTTAAGATA
TTTTTCTGAAGGTTGCCCAGGGCACAAACAAATTGGACACTTTCACTGCTAAAAAGTACA
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CTTTCATAAAATATGCAGATAAGAAGTGTTAAATGGGATTCAAGAATTATGGTTTTATTT
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AGTTTGGGGTGGTTTTTTGAAAACGAAACTGAAAAAAATTATATGTGAAAATGAGAACTG
GGTAAATAAAATTATATTTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAG

US 9,956,536 B2

FIG. 5

ATGTTCTTTCTACTTCATTTCATCGTTCTGATCAATGTCAAAGATTTTGCACTGACTCAA
GGTAGCATGATCACTCCTTCATGCCAAAAAGGATATTTTCCCTGTGGGAATCTTACCAAG
TGCTTACCCCGAGCTTTTCACTGTGATGGCAAGGATGACTGTGGGAACGGGGCGGACGAA
GAGAACTGTGGTGACACTAGTGGATGGGCGACCATATTTGGCACAGTGCATGGAAATGCT
AACAGCGTGGCCTTAACACAGGAGTGCTTTCTAAAACAGTATCCACAATGCTGTGACTGC
AAAGAAACTGAATTGGAATGTGTAAATGGTGACTTAAAGTCTGTGCCGATGATTTCTAAC
AATGTGACATTACTGTCTCTTAAGAAAAACAAAATCCACAGTCTTCCAGATAAAGTTTTC
ATCAAATACACAAAACTTAAAAAGATATTTCTTCAGCATAATTGCATTAGACACATATCC
AGGAAAGCATTTTTTGGATTATGTAATCTGCAAATATTAATTCTAGATGACAATCCAATA
ACCAGAATTTCACAGCGCTTGTTTACGGGATTAAATTCCTTGTTTTTCCTGTCTATGGTT
AATAACTACTTAGAAGCTCTTCCCAAGCAGATGTGTGCCCAAATGCCTCAACTCAACTGG
GTGGATTTGGAAGGCAATAGAATAAAGTATCTCACAAATTCTACGTTTCTGTCGTGCGAT
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TTGACGGACGGCATTTCTTCATTTGAGGACCTCTTGGCTAACAATATCCTCAGAATATTT
GTCTGGGTTATAGCTTTCATTACCTGCTTTGGAAATCTTTTTGTCATTGGCATGAGATCT
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TGCCTGATGGGTGTTTACTTGTTCTTTGTTGGCATTTTCGATATAAAATACCGAGGGCAG
TATCAGAAGTATGCCTTGCTGTGGATGGAGAGCGTGCAGTGCCGCCTCATGGGGTTCCTG
GCCATGCTGTCCACCGAAGTCTCTGTTCTGCTACTGACCTACTTGACTTTGGAGAAGTTC
CTGGTCATTGTCTTCCCCTTCAGTAACATTCGACCTGGAAAACGGCAGACCTCAGTCATC
CTCATTTGCATCTGGATGGCGGGATTTTTAATAGCTGTAATTCCATTTTGGAATAAGGAT
TATTTTGGAAACTTTTATGGGAAAAATGGAGTATGTTTCCCACTTTATTATGACCAAACA
GAAGATATTGGAAGCAAAGGGTATTCTCTTGGAATTTTCCTAGGTGTGAACTTGCTGGCT
TTTCTCATCATTGTGTTTTCCTATATTACTATGTTCTGTTCCATTCAAAAAACCGCCTTG
CAGACCACAGAAGTAAGGAATTGTTTTGGAAGAGAGGTGGCTGTTGCAAATCGTTTCTTT
TTTATAGTGTTCTCTGATGCCATCTGCTGGATTCCTGTATTTGTAGTTAAAATCCTTTCC
CTCTTCCGGGTGGAAATACCAGACACAATGACTTCCTGGATAGTGATTTTTTTCCTTCCA
GTTAACAGTGCTTTGAATCCAATCCTCTATACTCTCACAACCAACTTTTTTAAGGACAAG
TTGAAACAGCTGCTGCACAAACATCAGAGGAAATCAATTTTCAAAATTAAAAAAAAAAGT
TTATCTACATCCATTGTGTGGATAGAGGACTCCTCTTCCCTGAAACTTGGGGTTTTGAAC
AAAATAACACTTGGAGACAGTATAATGAAACCAGTTTCCTAG

US 9,255,139 B2

FIG. 6

MFFLLHFIVLINVKDFALTQGSMITPSCQKGYFPCGNLTKCLPRAFHCDGKDDCGNGADE
ENCGDTSGWATIFGTVHGNANSVALTQECFLKQYPQCCDCKETELECVNGDLKSVPMISN
NVTLLSLKKNKIHSLPDKVFIKYTKLKKIFLQHNCIRHISRKAFPGLCNLQILILDDNPI
TRISQRLFTGLNSLFFLSMVNNYLEALPKQMCAQMPQLNWVDLEGNRIKYLTNSTFLSCD
SLTVLFLPRNQIGFVPEKTFSSLKNLGELDLSSNTITELSPHLFKDLKLLQKLNLSSNPL
MYLHKNQPESLKQLQSLDLERIEIPNINTRMFQPMKNLSHIYFKNFRYCSYAPHVRICMP
LTDGISSFEDLLANNILRIFVWVIAFITCFGNLFVIGMRSFIKAENTTHAMSIKILCCAD
CLMGVYLFFVGIFDIKYRGQYQKYALLWMESVQCRLMGFLAMLSTEVSVLLLTYLTLEKF
LVIVFPFSNIRPGKRQTSVILICIWMAGFLIAVIPFWNKDYFGNFYGKNGVCFPLYYDQT
EDIGSKGYSLGIFLGVNLLAFLIIVFSYITMFCSIQKTALQTTEVRNCFGREVAVANRFF
FIVFSDAICWIPVFVVKILSLFRVEIPDTMTSWIVIFFLPVNSALNPILYTLTTNFFKDK
LKQLLHKHQRKSIFKIKKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIMKPVS

FIG. 7

MFFLLHFIVL INVKDFALTQ GSMITPSCQK GYFPCGNLTK CLPRAFHCDG
KDDCGNGADE ENCGDTSGWA TIFGTVHGNA NSVALTQECF LKQYPQCCDC
KETELECVNG DLKSVPMISN NVTLLSLKKN KIHSLPDKVF IKYTKLKKIF
LQHNCIRHIS RKAFPGLCNL QILYLNHNCI TTLRPGIFKD LHQLTWLILD
DNPITRISQR LFTGLNSLFF LSMVNNYLEA LPKQMCAQMP QLNWVDLEGN
RIKYLTNSTF LSCDSLTVLF LPRNQIGFVP EKTFSSLKNL GELDLSSNTI
TELSPHLFKD LKLLQKLNLS SNPLMYLHKN QFESLKQLQS LDLERIEIPN
INTRMFQPMK NLSHIYFKNF RYCSYAPHVR ICMPLTDGIS SFEDLLANNI
LR**IFVWVIAF ITCFGNLFVI GM**RSFIKAEN TTHAMSIK**IL CCADCLMGVY**
LFFVGIFDIK YRGQYQKYAL LWMESVQCR**L MGFLAMLSTE VSVLLLTYLT**
LEKFLVIVFP FSNIRPGKRQ TS**VILICIWM AGFLIAVIPF W**NKDYFGNFY
GKNGVCFPLY YDQTEDIGSK GYS**LGIFLGV NLLAFLIIVF SYITMFC**SIQ
KTALQTTEVR NCFGREVAVA NR**FFFIVFSD AICWIPVFVV KILSLF**RVEI
PDTMTSW**IVI FFLPVNSALN PILYTLT**TNF FKDKLKQLLH KHQRKSIFKI
KKKSLSTSIV WIEDSSSLKL GVLNKITLGD SIMKPVS

FIG. 8A

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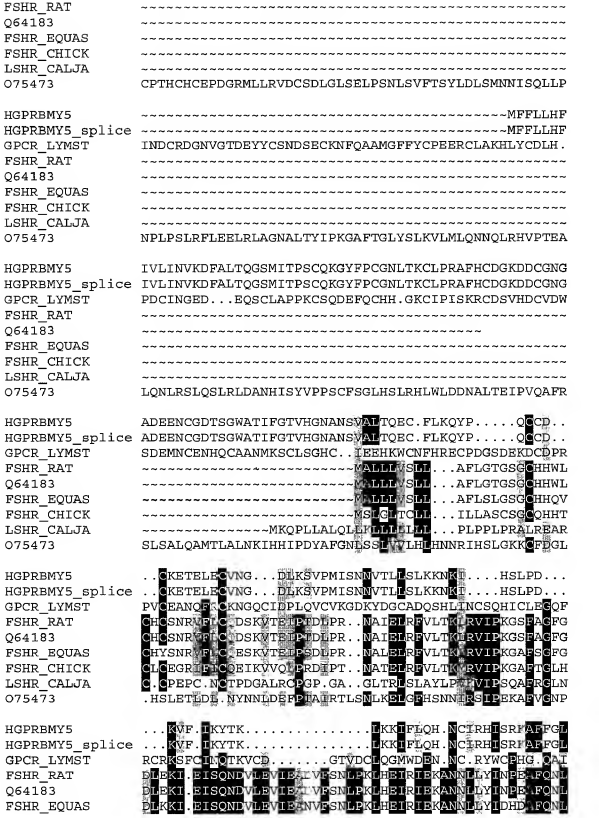
HGPRBMY5          ~~~
```

FIG. 8B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Q64183
FSHR_EQUAS
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GPCR_LYMST
FSHR_RAT
Q64183
FSHR_EQUAS
FSHR_CHICK
LSHR_CALJA
O75473
HGPRBMY5
HGPRBMY5_splice
GPCR_LYMST
FSHR_RAT
Q64183
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O75473
HGPRBMY5
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GPCR_LYMST
FSHR_RAT
Q64183
FSHR_EQUAS
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FSHR_RAT
Q64183
FSHR_EQUAS

FIG. 8C

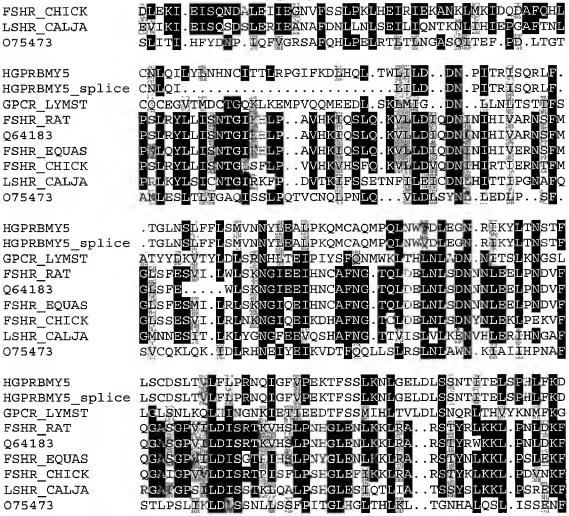

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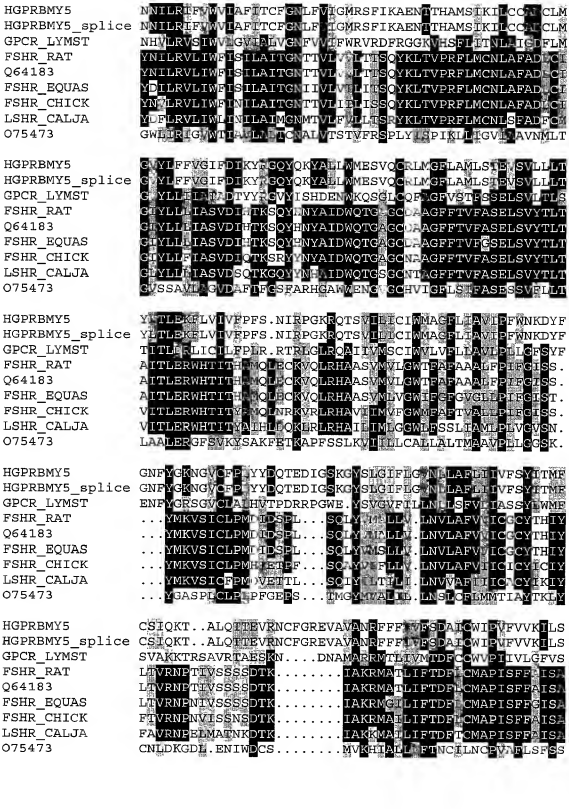
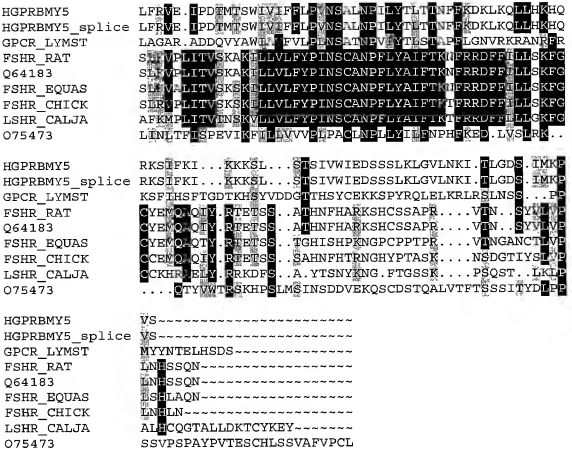
Fig. 8D



US 2003/0224361 A1

FIG. 8E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HGPRBMY5_splice
GPCR_LYMST
FSHR_RAT
Q64183
FSHR_EQUAS
FSHR_CHICK
LSHR_CALJA
O75473

FIG. 9A

```
  1 MFFLLHFIVLINVKDFALTQGSMITPSCQKGYFPCGNLTKCLPRAFHCDG 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MFFLLHFIVLINVKDFALTQGSMITPSCQKGYFPCGNLTKCLPRAFHCDG 50

 51 KDDCGNGADEENCGDTSGWATIFGTVHGNANSVALTQECFLKQYPQCCDC 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 KDDCGNGADEENCGDTSGWATIFGTVHGNANSVALTQECFLKQYPQCCDC 100

101 KETELECVNGDLKSVPMISNNVTLLSLKKNKIHSLPDKVFIKYTKLKKIF 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 KETELECVNGDLKSVPMISNNVTLLSLKKNKIHSLPDKVFIKYTKLKKIF 150

151 LQHNCIRHISRKAFFGLCNLQILYLNHNCITTLRPGIFKDLHQLTWLILD 200
    ||||||||||||||||||||||                  ||||
151 LQHNCIRHISRKAFFGLCNLQI.....................LILD 176

201 DNPITRISQRLFTGLNSLFFLSMVNNYLEALPKQMCAQMPQLNWVDLEGN 250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
177 DNPITRISQRLFTGLNSLFFLSMVNNYLEALPKQMCAQMPQLNWVDLEGN 226

251 RIKYLTNSTFLSCDSLTVLFLPRNQIGFVPEKTFSSLKNLGELDLSSNTI 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
227 RIKYLTNSTFLSCDSLTVLFLPRNQIGFVPEKTFSSLKNLGELDLSSNTI 276

301 TELSPHLFKDLKLLQKLNLSSNPLMYLHKNQFESLKQLQSLDLERIEIPN 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
277 TELSPHLFKDLKLLQKLNLSSNPLMYLHKNQFESLKQLQSLDLERIEIPN 326

351 INTRMFQPMKNLSHIYFKNFRYCSYAPHVRICMPLTDGISSFEDLLANNI 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
327 INTRMFQPMKNLSHIYFKNFRYCSYAPHVRICMPLTDGISSFEDLLANNI 376

401 LRIFVWVIAFITCFGNLFVIGMRSFIKAENTTHAMSIKILCCADCLMGVY 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
377 LRIFVWVIAFITCFGNLFVIGMRSFIKAENTTHAMSIKILCCADCLMGVY 426

451 LFFVGIFDIKYRGQYQKYALLWMESVQCRLMGFLAMLSTEVSVLLLTYLT 500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
427 LFFVGIFDIKYRGQYQKYALLWMESVQCRLMGFLAMLSTEVSVLLLTYLT 476

501 LEKFLVIVFPFSNIRPGKRQTSVILICIWMAGFLIAVIPFWNKDYFGNFY 550
    ||||||||||||||||||||||||||||||||||||||||||||||||||
477 LEKFLVIVFPFSNIRPGKRQTSVILICIWMAGFLIAVIPFWNKDYFGNFY 526

551 GKNGVCFPLYYDQTEDIGSKGYSLGIFLGVNLLAFLIIVFSYITMFCSIQ 600
    ||||||||||||||||||||||||||||||||||||||||||||||||||
527 GKNGVCFPLYYDQTEDIGSKGYSLGIFLGVNLLAFLIIVFSYITMFCSIQ 576
```

US 2003/0232350 A1

FIG. 9B

```
601 KTALQTTEVRNCFGREVAVANRFFFIVFSDAICWIPVFVVKILSLFRVEI 650
    ||||||||||||||||||||||||||||||||||||||||||||||||||
577 KTALQTTEVRNCFGREVAVANRFFFIVFSDAICWIPVFVVKILSLFRVEI 626

651 PDTMTSWIVIFFLPVNSALNPILYTLTTNFFKDKLKQLLHKHQRKSIFKI 700
    ||||||||||||||||||||||||||||||||||||||||||||||||||
627 PDTMTSWIVIFFLPVNSALNPILYTLTTNFFKDKLKQLLHKHQRKSIFKI 676

701 KKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIMKPVS 737
    |||||||||||||||||||||||||||||||||||||
677 KKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIMKPVS 713
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T09260 "9E559660

FIG. 10

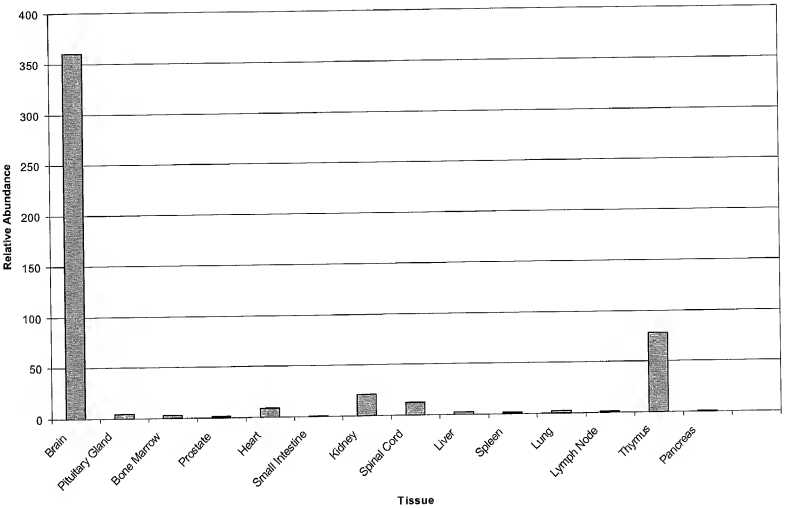
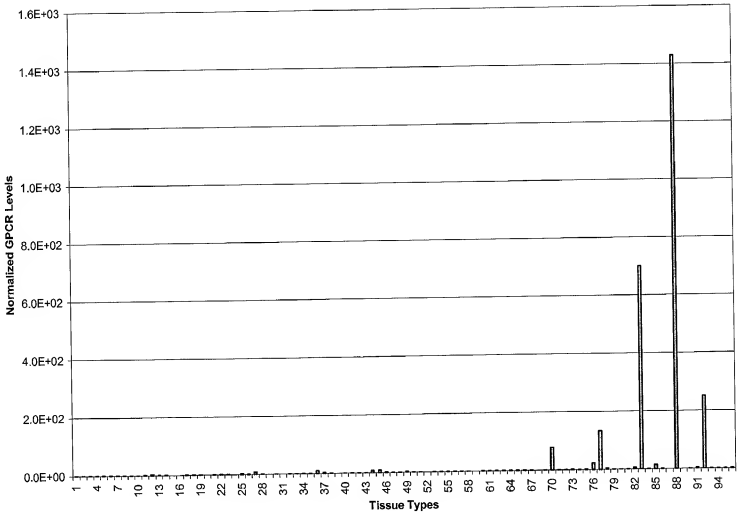


FIG. 11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1.4E+03
1.2E+03
1.0E+03
8.0E+02
6.0E+02
4.0E+02
2.0E+02
0.0E+00
Normalized GPCR Levels
1
4
7
10
13
16
19
22
25
28
31
34
37
40
43
46
49
52
55
58
61
64
67
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76
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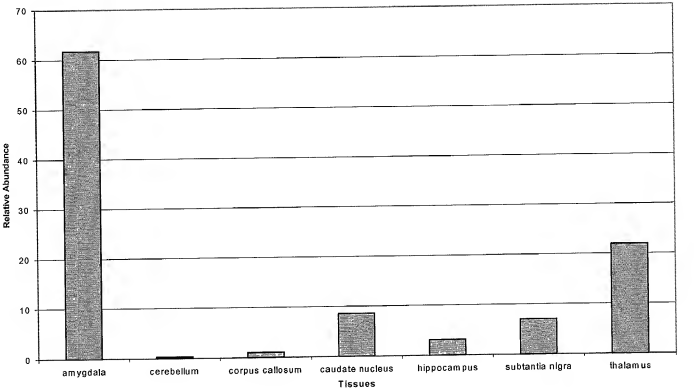
82
85
88
91
94
Tissue Types

FIG. 12


70
60
50
40
30
20
10
0
Relative Abundance
amygdala
cerebellum
corpus callosum
caudate nucleus
hippocampus
subtantia nigra
thalamus
Tissues